**BONUS WRITING**

Yet the reviewers were exactly right when they criticized the skeptical outlook of the authors vis-à-vis the fossil record, and we believe that the publication of Thompson and Ramirez-Barahona (2023) is symptomatic of a potential problem in which many comparative biologists are unjustifiably mistrustful of fossil evidence and insufficiently critical of evidence based on extant taxa.

In the plant biology world, debate about the relative merits of fossil evidence vs. phylogenetic analysis has largely been centered around estimates of the origin of angiosperms, where molecular clock analyses based on extant taxa frequently estimate much earlier origination times than fossil evidence (see Coiro et al. 2019). On this front, the trustworthiness of the fossil record has been aggressively defended (see Herendeen et al. 2017), whereas molecular clock research is, by the admission of its architects, still evolving (e.g., Smith et al. 2010; Beaulieu et al. 2015; Brown and Smith 2018). In diversification research, while few would argue that we should abandon phylogeny-based diversification rate estimates with ones gleaned from the fossil record, a related debate is currently underway regarding our ability to uncover identifiable diversification histories (Louca and Pennell 2020; Helmstetter et al. 2022). To our knowledge, a debate specifically surrounding mass extinction estimates from phylogenies has not been had. This may be because, while cryptic mass extinction events have been inferred from phylogenies (e.g., Crisp and Cook 2009; Magee and Höhna 2021), we believe that Thompson and Ramirez-Barahona (2023) is the first study to argue *against* a mass extinction using evidence from phylogenies.

For decades, comparative biology has been a contentious field beset by issues (see Hull 1988). Concerns are frequently raised about the accuracy of our methods (e.g., Rabosky 2010; Rabosky and Goldberg 2015; Louca and Pennell 2020) and the ability of practitioners to accurately use them (e.g., Cooper et al. 2016; Begum and Robinson-Rechavi 2021). This response to Thompson and Ramirez-Barahona certainly falls into this quasi-genre, though we are perennially skeptical of many criticisms of comparative methods (see Harvey et al. 1995; Beaulieu and O’Meara 2016; Grabowski et al. 2023). Therefore, we do not want to end on a simplistic note along the lines of “practitioners need to be more careful when using methods with complex underpinnings.” We wish to meditate on a more interesting problem: what can comparative methods potentially tell us about evolution?

The answer lies somewhere between Thompson and Ramirez-Barahona, who clearly think molecular phylogenies retain excellent information about the distant past, and someone like Brower (2018), who, like many members of the “old man yells at cloud” school of systematic biology, seems to believe that any model other than parsimony will produce a useless tree. Perhaps their findings would have been assisted by methods that account for fossils (Quental and Marshall 2010; but see Beaulieu and O’Meara 2023), or generally striving to include many different streams of evidence to attack single problems (Donoghue and Edwards 2019; Gardner and Organ 2021).

It may be true that more phylogenetic knowledge is required for biologists, or at least those who conduct peer review of papers that employ phylogenetic methods. An examination of the review history for Thompson and Ramirez-Barahona (2023) reveals that a reviewer (both were paleobiologists) did, in fact, argue that TESS + CoMET may not be an appropriate method in light of its disagreement with the fossil record. But his comment did not mention the fact that the authors of those methods said that their method cannot reliably infer ancient mass extinctions, and he seemed somewhat phylogenetically illiterate.

For years, comparative biologists have struggled with what to make of the fossil record (see Morlon et al. 2011). In the frequent cases when rate calculations, divergence time estimates, and other inferences from molecular phylogenies disagree with evidence in the fossil record, one is forced to choose a side. While we fault Thompson and Ramirez-Barahona (2023) for flaws in their analyses, they are not the first to choose the side of PCMs over fossils, and convincing cases can certainly be made. Smith et al. (2010) analyzed the divergence times of a phylogeny of 154 land plant species and estimated that flowering plants originated during the Late Triassic approximately 217 mya, much earlier than the earliest known angiosperm fossils dating to about 130 mya (Gomez et al. 2015; Coiro et al. 2019). They argued that the almost 100-million-year gap between estimated origin and first fossils could be caused by early angiosperms being geographically restricted and ecologically insignificant prior to the Late Cretaceous.

However, later analyses incorporating rate heterogeneity suggested that the Triassic origin was indeed an overestimate (Beaulieu et al. 2015), and current efforts to date the divergence of angiosperms often explicitly intend to move the root closer to the Late Cretaceous (e.g., Brown and Smith 2018). Many of the most exciting avenues in the world of PCMs aim to integrate fossils and phylogenies (e.g., Heath et al. 2014; Mitchell et al. 2019) rather than pit them against each other, signaling a shift from viewing the fossil record as biased and unreliable to an invaluable resource. This is a good thing: while molecular phylogenies do contain valuable information that must be analyzed with tools like TESS and CoMET, one cannot in good conscience “disprove” paleontological evidence with phylogenetic evidence.

Since time-calibrated molecular phylogenies are models of lineage accumulation through time, this point can be analogized to a problem in the earth sciences described by Oreskes et al. (1994).

Thompson and Ramirez-Barahona carefully titled their paper “No evidence for angiosperm mass extinction at the Cretaceous-Palaeogene (K-Pg) boundary,” presumably to avoid the “appeal to ignorance” fallacy, summed up by the phrase “absence of evidence is not evidence of absence.” However, they fall into the fallacy by arguing that the phylogenetic evidence demonstrates the resilience of angiosperms.

* Fossil adding thing:
  + LTT plots can show very different results when a hypothetical tree has extinct taxa removed (like a normal one for a molecular phylogeny) vs. when extinct taxa are retained (Marshall 2017)
  + Sepkoski (1975) suggests that survivorship curves [is this relevant?] can be accurate with just 20% of fossils discovered
  + We stress-tested TESS by gradually removing extinct taxa from the phylogeny to see model results would change
  + Even adding fossils to the tree does not do basically anything (show numbers)